

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2002, 17:32:26 ; Search time 37.53 Seconds
(without alignments)
540.230 Million cell updates/sec

Title: US-09-502-984B-6

Perfect score: 1098

Sequence: 1 KFSKALALAAKPEELICF.....AEPFGGFWAMSEPVSLTR 211

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1060	96.5	508	1	ZUHUR erythropoietin rec
2	877.5	79.9	507	1	A46713 erythropoietin rec
3	869.5	79.2	265	2	S14081 erythropoietin rec
4	869.5	79.2	507	1	A32385 erythropoietin rec
5	171	15.6	625	2	S35317 hematopoietic grow
6	164	14.9	626	2	S37622 proto-oncogene - m
7	146	13.3	579	2	B45266 MPL-K protein prec
8	146	13.3	635	2	A45266 MPL-K protein prec
9	118	10.7	581	2	I45971 prolactin receptor
10	111	10.1	522	2	B45268 interleukin-9 rece
11	110.5	10.1	634	2	S33339 somatotropin recep
12	107	9.7	608	2	S32823 somatotropin recep
13	104	9.5	616	2	A30304 prolactin receptor
14	103.5	9.4	677	2	S33608 somatotropin-bind
15	103.5	9.4	831	2	UQ1655 prolactin receptor
16	103	9.4	638	2	S12136 somatotropin recep
17	99.5	9.1	638	2	B28176 somatotropin recep
18	98.5	9.0	830	2	I50455 prolactin receptor
19	98	8.9	897	1	A39255 cytokine receptor
20	96.5	8.8	378	2	A40265 interleukin-3 rece
21	94	8.6	468	2	A45268 interleukin-9 rece
22	92.5	8.4	279	2	B32985 somatotropin-bind
23	92.5	8.4	638	2	A33505 somatotropin recep
24	92	8.4	2594	2	A35774 kinase-related pro
25	91	8.3	292	2	I77525 prolactin receptor
26	91	8.3	303	2	I77524 prolactin receptor
27	91	8.3	608	2	I53269 prolactin receptor
28	89.5	8.2	467	2	I56896 gene gfi-2 protein
29	88	8.0	288	2	B59405 prolactin receptor

30	88	8.0	376	2	A59405 prolactin receptor
31	88	8.0	622	2	A40144 prolactin receptor
32	87.5	8.0	1825	2	C68400 protein H19M22.1-1
33	87.5	8.0	1825	2	T32828 hypothetical prote
34	87	7.9	910	2	A25884 prolactin receptor
35	87	7.9	412	2	A41070 prolactin receptor
36	87	7.9	610	2	A34631 prolactin receptor
37	87	7.9	610	2	A36116 prolactin receptor
38	86	7.8	61	2	I38208 erythropoietin rec
39	85.5	7.8	863	2	H87556 aminopeptidase N l
40	85	7.7	284	2	S27931 Env/v-mpl fusion p
41	84	7.7	486	1	K1BYHB hexokinase (EC 2.7
42	83.5	7.6	1097	2	S17308 leukemia inhibitor
43	83	7.6	976	2	A36355 protein-tyrosine k
44	82.5	7.5	378	2	AF3320 flavohemoprotein l
45	82	7.5	336	2	I49581 CD1.1 - mouse

ALIGNMENTS

RESULT 1

ZUHUR
C:Species: Homo sapiens (man)
C:Date: 12-Feb-1993 #sequence.revision 05-Apr-1995 #extl.change 22-Jun-1999
C:Accession: A43799; A60160; A49824; A53958; A55280; I52563
R:Jones, S.S.; D'Andrea, A.D.; Haines, L.L.; Wong, G.G.
Blood 76, 31-35, 1990
A>Title: Human erythropoietin receptor: cloning, expression, and biologic characteriz
A:Reference number: A43799; MUID:90304340
A:Accession: A43799

A:Molecule type: mRNA
A:Residues: 1-508 <CON>
A:Cross-references: GB:M60459; NID:9182244; PIDN:AAA52403.1; PID:9182245
R:Winkelmann, J.C.; Penny, L.A.; Deaven, L.L.; Forget, B.G.; Jenkins, R.B.
Blood 76, 24-30, 1990
A>Title: The gene for the human erythropoietin receptor: analysis of the coding seque
A:Reference number: A60160; MUID:90304334
A:Accession: A60160

A:Status: not compared with conceptual translation
A:Molecule type: mRNA; DNA
A:Residues: 1-101, 'R', 103-188, 'RP', 191-243, 'E', 245-508 <MIN>
R:Noguchi, C.T.; Bae, K.S.; Chiu, K.; Wada, Y.; Schechter, A.N.; Hankins, W.D.
Blood 78, 2548-2556, 1991
A>Title: Cloning of the human erythropoietin receptor gene.
A:Reference number: A49824; MUID:9239733
A:Accession: A49824

A:Molecule type: DNA
A:Residues: 1-508 <NOG>
A:Cross-references: GB:S45332; NID:9255496; PIDN:AA823271.1; PID:9255497
A:Experimental source: Placenta
A>Note: Sequence extracted from NCBI backbone (NCBIN:113293, NCBIPI:113294)
R:Ehrenman, K.; St. John, T.
Exp. Hematol. 19, 973-977, 1991
A>Title: The erythropoietin receptor gene: cloning and identification of multiple tra
A:Reference number: A53958; MUID:91372559
A:Accession: A53958

A:Molecule type: mRNA
A:Residues: 1-508 <EHR>
R:Penny, L.A.; Forget, B.G.
Genomics 11, 974-980, 1991
A>Title: Genomic organization of the human erythropoietin receptor gene.
A:Reference number: A55280; MUID:92147143
A:Accession: A55280

A:Molecule type: DNA
A:Residues: 1-17, 381-387, 'LLEQQQDA', 391-395, 504-508 <PEN>
A>Note: Sequence modified after extraction from NCBI backbone
A>Note: The authors translated the codon GAT for residue 31 as B
R:Maouche, L.; Tournamille, C.; Hattab, C.; Boffa, G.; Carton, J.P.; Chretien, S.
Blood 78, 2557-2563, 1991
A>Title: Cloning of the gene encoding the human erythropoietin receptor.

A:Reference number: 152563; MUID:92399734
A:Accession: 152563
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1..96 <RES>
A:Cross-references: GB:M76595; NID:g182147; PIDN:AAA5239.1; PID:g553281
C:Genetics:
A:Gene: GDB:EPOR
A:Cross-references: GDB:125242; OMIM:133171
A:Map position: 19p13.3-19p13.2
A:Introns: 39/1; 84/2; 143/1; 195/3; 247/1; 276/2; 305/3
C:Superfamily: erythropoietin receptor; cytokine receptor homology
C:Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-508/Product: erythropoietin receptor #status predicted <MAT>
F:52-250/Domain: extracellular #status predicted <EXT>
F:52-239/Domain: cytokine receptor homology <CRS>
F:233-237/Region: WSXWS motif
F:251-272/Region: transmembrane #status predicted <TM>
F:273-508/Domain: intracellular #status predicted <INT>
F:52-62..91-107/Disulfide bonds: #status predicted
F:76/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match	96.5%	Score 1060	DB 1	Length 508
Best Local Similarity	93.8%	Pred. No. 5.4e-95		
Matches 198, Conservative	11	Mismatches 2	Indels 0	Gaps 0

OY	1	KEESFAALLAARGBELLICFERLEDIVCFPEEASAGVGVGNNSFFOFLEDEPMKICRL	60
Db	34	KFEESFAALLAARGBELLICFERLEDIVCFMEEASAGVGVGNNSFFOFLEDEPMKICRL	93
OY	61	HOAPTARGAIRFMCSSLPTADTSSEFVPELELRTLAASGAPRPHRVHINEVULLDAPVLA	120
Db	94	HOAPTARGAVAFMCSSLPTADTSSEFVPELELRTLAASGAPRPHRVHINEVULLDAPVLA	153
OY	121	RLADESGHVIVRMLPPEPTPMTSHIRREBLDISAGNGAGSVORVELLEGRTECVLSNLGR	180
Db	154	RLADESGHVIVRMLPPEPTPMTSHIRREVDVSAANGAGSVORVELLEGRTECVLSNLGR	213
OY	181	TRITIAVARMAAEPSPFGGFWMSAMEEPPSLLT	211
Db	214	TRITIAVARMAAEPSPFGGFWMSAMEEPPSLLT	244

RESULT
A46713

erythropoietin receptor precursor - rat
C:Species: Rattus norvegicus (Norway rat)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: A46713

Ramasuda, S.; Nagao, M.; Takahata, K.; Konishi, Y.; Gallyas Jr., F.; Tablira, T.; Sasak, J. *Biol. Chem.* 268, 11208-11216, 1993

A1: Title: Functional erythropoietin receptor of the cells with neural characteristics. C
A: Reference number: A46713; MUID: 3326574

A;Accession: A46713
A;Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-507 <MAS>

A/Cross-references: GB: D135566; NID: g286209; PIDN: BAA02761.1; PID: g286210
A/Experimental source: PC12 and erythroid cells

A: Note: sequence extracted from NCBI backbone (NCBIN:132811, NCBI:P:132813)
C: Superfamily: erythropoietin receptor; cytokine receptor homology

C;Keywords: cytokine receptor; glycoprotein; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <Sig>

F;25-507/Product: erythropoietin receptor #status predicted
F;25-249/Domain: extracellular #status predicted <EXT>

F;52-238/Domain: cytokine receptor homology <CRS>
F;250-271/Domain: transmembrane #status predicted

F;272-507/Domain:	intracellular	#status	predicted	<INT>
F;75/Binding site:	carbohydrate (Asn) (covalent)	#status	predicted	

Query Match	79.9%	Score 877.5;	DB 1;	Length 507;
Best Local Similarity	78.2%;	Pred. No. 2.9e-77;		
Matches 165;	Conservative 23;	Mismatches 22;	Indels 1;	Gaps 1.

```
OY      1 KFSKSAALLARGBEELLCFERREDIVCFPEEAASAGVGRGNSSFEQLEDEBPKIKCRL    60
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      34 KFESKAALLARSGSEELLCFTQRLEDIVCFMEEEAANSNGM- FNTSFSTOLEGESRKSCL    92
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      61 HOAPTARGAIRFWCSLPTADTSSFVPLELRITLAASGAPRFPRVTHINEVVLLDPAQGLVA   120
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      93 HQAPTRGSMSMFWSLPTADTSSFPLELTQTEASGSPRYHRIIHINEVLLDAPAGLLA   152
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      121 RLADESGHVIRKLPPRETPMTSHIREBLDSAGNGAGSVQRYELLEGRFECVLNIGRR    180
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      153 RRAEGSSHVIRKLPPAPALMTTIIRIEVDVASGNRRAGGTQRYVEVLEGRTCYLSNLRG    212
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      181 TRITIAVARMAEPSCFGFNAMSEPSLTT    211
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      213 TRYTFAVARAAMEPSCFGFNAMSEPSLTT    243
```

RESULT
S14081

erythropoietin receptor - mouse
C;Species: Mus musculus (house mouse)

C:date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S14081; T49653

R; Kuramochi, S.; Ikawa, Y.;
J. Mol. Biol. 216, 567-575,
1993.

A/Title: Characterization of murine erythropoietin receptor genes:
A/Reference number: S13249; MUID:91080149
A/Accession number: 514081

A;Accession: 514061
A;Status: preliminary
A;Molecular Weight: 40000

A/molecule type: DNA
A/Residues: 1-265 <KUR>

Ribascombe, C., Chénierien, S., Bellard-Chanvot, V., Mayeux, F., J. Biol. Chem. 266, 6952-6956, 1991

A:Reference number: I49653; MUID:91201346
A:Accession: I49653

A;accession: 149053
A;status: preliminary
A;notes: 4 pages. On

A; Residues: 1-24 <RES>
A; Molecule type: UNA
A; CSD: CSD-MC3260, NTD: 0103100, PTD: 0103200

Cytokine receptor homology
cytokine receptor
erythropoietin receptor
superfamily:
receptor
transmembrane protein
cell surface
ligand

F;52-238/Domain: cytokine receptor homology <CRS>

Quarry Match DB 3: Length 265
70 38: Score 860 5:

Query match	13.2%	Score	809.9	DB	2	Length	200
Best Local Similarity	77.7%	Pred. No.	7.7e-77				
Matches	164	Conservatism	33	Mismatches	24	Indels	1
							1

Category	Count	Percentage
Matched	104	27%
Mismatches	27	7%
Conservative	24	6%
Neutral	1	0%
Gap	1	0%

1 KFEESAAHLLAARGPEELLCE I ERLEEDVCF EELAAASAVGPGNCF SF QVDEDEEEMULAL

24 VEEVCAAT KACPGGRII CEMOPI EDI VCEMEEAACCGM -DENGEENVOI ECEEGRCOSI

34 АПСНААИЛАНСОНСЕЛЛУО I QUNNEUVC WEEMASOM - DEINIZI QI QUNNEONANNOLO 32

01	HOA1IARGAINTWCSLEFIANJ55FVLELUNLIAMSGNFNF	NRV	RT	IN	EV	LD	DAF	VG	VA	120
02										121
03										122
04										123
05										124
06										125
07										126
08										127
09										128
10										129
11										130
12										131
13										132
14										133
15										134
16										135
17										136
18										137
19										138
20										139
21										140
22										141
23										142
24										143
25										144
26										145
27										146
28										147
29										148
30										149
31										150
32										151
33										152
34										153
35										154
36										155
37										156
38										157
39										158
40										159
41										160
42										161
43										

103 93 HQBPIVKGSVKWCSPJADJISF VPLEBQVI EASGSFRI HRIIHNINEV LDDAFAGDUA 132

[illegible]

DD	153	KRAEGSHVLEWLPBPAGAMTHIKRIEVDVSAGNKGAGIQRYEVLGRIECLVSNLKG	212
CC	101	MDTETAIIDADMDPDCTGCGGAGNAGHCHRVCLIT	211

qy	161	IKI.IAVKAKMAEPFSGUWMSAMSEPVSLII	ZII
qz	11		
sh	313	EBVBNHURPNUZBDBNCCGCGTICNDPQRTM	243

DD 213 IKIIFAVKAKMAERFSFGIWSAMSEFADLLI 243

RESULT 4

A32385 erythropoietin receptor precursor, membrane-bound form - mouse

```

C:Species: Mus musculus (house mouse)
C:Date: 28-Sep-1990 #sequence_revision 05-Apr-1995 #text_change 22-Jun-1999
C:Accession: A41666; A32385; S13249
R:Hiho, M.; Tojo, A.; Misawa, Y.; Morii, H.; Takaku, F.; Shibuya, M.
Mol. Cell. Biol. 11, 5527-5533, 1991
A:Title: Unregulated expression of the erythropoietin receptor gene caused by insertion
A:Reference number: A41666; MUID:92017832
A:Accession: A41666
A:Molecule type: mRNA
A:Residues: 1-507 <HIN>
A:Cross-references: GB:S59388; NID:g237036; PIDN:AAB20029.1; PID:g237037
A:Experimental source: murine erythro leukemia (MEL) cell line F5-5
R:D'Andrea, A.D.; Lodish, H.F.; Wong, G.G.
Cell 57, 277-285, 1989
A:Title: Expression cloning of the murine erythropoietin receptor.
A:Reference number: A32385; MUID:89195238
A:Accession: A32385
A:Molecule type: mRNA
A:Residues: 1-507 <DNA>
A:Cross-references: GB:004843; NID:g193090; PIDN:AAA37571.1; PID:g309219
A:Experimental source: murine erythro leukemia (MEL) cells, subclone 745
R:Kuramochi, S.; Ikawa, Y.; Todokoro, K.
J. Mol. Biol. 216, 567-575, 1990
A:Title: Characterization of murine erythropoietin receptor genes.
A:Reference number: S13249; MUID:91080149
A:Accession: S13249
A:Molecule type: DNA; mRNA
A:Residues: 1-507 <KUR>
A:Cross-references: EMBL:X53081; NID:g50861; PIDN:CAA37248.1; PID:g50862
A:Experimental source: murine erythro leukemia K-1 cells
C:Genetics:
A:Introns: 39/1; 83/2; 142/1; 194/3; 246/1; 275/2; 304/3
C:Superfamily: erythropoietin receptor; cytokine receptor homology
C:Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-507/Product: erythropoietin receptor #status predicted <MAT>
F:25-246/Domain: extracellular #status predicted <EXT>
F:250-238/Domain: cytokine receptor homology <CRS>
F:250-271/Domain: transmembrane #status predicted <TMN>
F:272-507/Domain: intracellular #status predicted <INT>
F:52-62, 90-106/Disulfide bonds: #status predicted
F:75/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match          79.2%; Score 869.5; DB 1; Length 507;
Best Local Similarity 77.7%; Pred. No. 1,7e-76;
Matches 164; Conservative 22; Mismatches 24; Indels 1; Gaps 1;

QY 1 KFESKAALLAARGPELLCTERLEDLVCFEEAASAGVGPNGFSFQLEDEPMKLCRL 60
      |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 34 KFESKAALLAARGSELLCTQRLLEDLVCFWEAAASGM-DPNYSFSYQLGESKCSLSL 92
      |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 HOAPARAARATFQWCLPTADTSSFYPLELRTAASGARFRFRVHINIVLLDAPVGLA 120
      |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 93 HOAPVAKRSVRFQWCSLPADTSSFYPLELQYTESGSRVHRIITHINIVLLDAPAGLA 152
      |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 121 RLADSGHVIVIRKMLPPETPMTHSHREFLDISAGNAGVQSVQVELLEGRCTCVSLNLRG 180
      |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 153 RRAEGSHVILRWLPPRAPAPMTHTHRYEVDVSAGNRAGGTQREYVLEBRTCTVSLNLRGG 212
      |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 181 TRITIAVARARNAEBSFGGFWSAMSEPVSLT 211
      |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 213 TRYFAVARARNAEBSFGGFWSAMSEPVSLT 243
      |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 5
S35317
hematopoietic growth factor receptor precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S35317; S35316
R:Skoda, R.C.; Seidlin, D.C.; Chiang, M.K.; Peichel, C.L.; Vogt, T.F.; Leder, P.
EMBO J. 12, 2645-2653, 1993

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A:Title: Murine c-mpl: a member of the hematopoietic growth factor receptor superfamily
A:Reference number: S35316; MUID:93327753
A:Accession: S35317
A:Molecule type: mRNA
A:Residues: 1-625 <SKO>
A:Cross-references: EMBL:222649; NID:g394725; PIDN:CAA80365.1; PID:g394726
A:Accession: S35316
A:Molecule type: DNA
A:Residues: 1-70 <SKW>
A:Cross-references: EMBL:222657
C:Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane prot
E:1-75/Domain: signal sequence #status predicted <Sig>
E:26-625/Product: hematopoietic growth factor receptor #status predicted <Mat>
E:26-482/Domain: extracellular #status predicted <Ext>
E:261-265/Region: WGXMS motif
E:463-469/Region: WSXMS motif
E:483-504/Domain: transmembrane #status predicted <TM>
E:505-625/Domain: intracellular #status predicted <Int>
F:113,117,178,349/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match          15.6%; Score 171; DB 2; Length 625;
Best Local Similarity 24.6%; Pred. No. 1.6e-08;
Matches 62; Conservative 33; Mismatches 105; Indels 52; Gaps 8;

OY      4 SKAALLARGPEELICTERLEDLVCFEEAASAGVPGNFSFQLEDEPMKLCRLHOA 63
       1:  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      25 SQDFVLLALGTEPLNCFSGQTFEDLTGCFWDEBEA--PSGTYYQLLYAVRGKPRACPLYSQ 82
       1:  | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY      64 PTARGAIREWCSLPTAD-TSSFVPLELRITPAAS-GARPRHRYHINEVLLADPAVGLVAR 121
       1:  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      83 SVPTGTTGYVCOFPAPQDEVRLEFPLHLWKNVSLNQTLIRVLEFVDSVGLPAPRYIKAR 142
       1:  | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY      122 LADSGHVIW-LPPETPMTSHIRELDI----SAGNGAGSVQVELLEGRT----- 170
       1:  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      143 GGSQGEELQIHWEAPAP--ISDFLRHRLRGPTDSSNATAPSV--IQLLSTECPTLW 198
       1:  | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY      171 -----ECVLSNLRGTRITIAVARAMEPSFG 197
       1:  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      199 MPNPVPLVDQPCVHPTASQHPGAPFLTWGSGCLVSGIQAASKSYMQLQRSQDGVSLR 258
       1:  | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY      198 GFMSANSPVSL 209
       1:  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      259 GSWGSPFPVTV 270
       1:  | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT      6
S37622
proto-oncogene - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S37622
R:Vignon, I.; Florindo, C.; Pichelson, S.; Guenet, J.L.; Mattei, M.G.; Souyri, M.; Cos
Oncogene 8, 2607-2615, 1993
A:Title: Characterization of the murine Mpl proto-oncogene, a member of the hematopoi
A:Reference number: S37622; MUID:93390934
A:Accession: S37622
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-626 <VIG>
A:Cross-references: EMBL:X73677; NID:g404318; PIDN:CAA52031.1; PID:g404319

Query Match          14.9%; Score 164; DB 2; Length 626;
Best Local Similarity 23.5%; Pred. No. 7.6e-08;
Matches 61; Conservative 34; Mismatches 105; Indels 60; Gaps 8;

OY      4 SKAALLARGPEELICTERLEDLVCFEEAASAGVPGNFSFQLEDEPMKLCRLHOA 63
       1:  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      18 SQDFVLLALGTEPLNCFSGQTFEDLTGCFWDEBEA--PSGTYYQLLYAVRGKPRACPLYSQ 75
       1:  | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY      64 PTARGAIREWCSLPT-ADTSEVPLELRITPAAS-GARPRHRYHINEVLLADPAVGLVAR 121
       1:  | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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